Full wwPDB EM Validation Report ⓘ

Oct 20, 2024 – 10:17 AM EDT

PDB ID	:	7LUE
EMDB ID	:	EMD-23521
Title	:	Prefusion RSV F glycoprotein bound by neutralizing site V-directed antibody ADI-14442
Authors	:	Gilman, M.S.A.; McLellan, J.S.
Deposited on	:	2021-02-22
Resolution	:	2.90 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

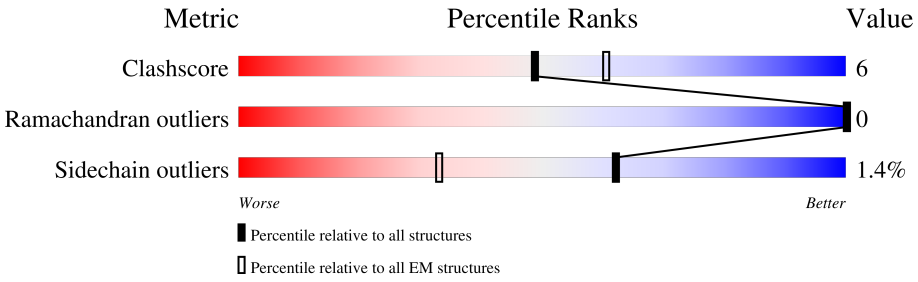
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	548	11% 65% 13% 22%
1	B	548	11% 64% 14% 22%
1	C	548	12% 64% 14% 22%
2	H	225	. 40% 8% 51%
2	I	225	5% 40% 9% 51%
2	J	225	5% 41% 8% 51%
3	L	219	8% 47% . 49%
3	M	219	8% 47% . 49%

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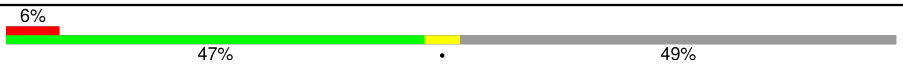
Mol	Chain	Length	Quality of chain
3	N	219	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 15018 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Fusion glycoprotein F0.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	427	Total	C	N	O	S	0	0
			3300	2086	542	652	20		
1	B	427	Total	C	N	O	S	0	0
			3300	2086	542	652	20		
1	C	427	Total	C	N	O	S	0	0
			3300	2086	542	652	20		

There are 189 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	66	GLU	LYS	conflict	UNP W8RJF9
A	67	ILE	ASN	engineered mutation	UNP W8RJF9
A	215	PRO	SER	engineered mutation	UNP W8RJF9
A	514	SER	-	expression tag	UNP W8RJF9
A	515	ALA	-	expression tag	UNP W8RJF9
A	516	ILE	-	expression tag	UNP W8RJF9
A	517	GLY	-	expression tag	UNP W8RJF9
A	518	GLY	-	expression tag	UNP W8RJF9
A	519	TYR	-	expression tag	UNP W8RJF9
A	520	ILE	-	expression tag	UNP W8RJF9
A	521	PRO	-	expression tag	UNP W8RJF9
A	522	GLU	-	expression tag	UNP W8RJF9
A	523	ALA	-	expression tag	UNP W8RJF9
A	524	PRO	-	expression tag	UNP W8RJF9
A	525	ARG	-	expression tag	UNP W8RJF9
A	526	ASP	-	expression tag	UNP W8RJF9
A	527	GLY	-	expression tag	UNP W8RJF9
A	528	GLN	-	expression tag	UNP W8RJF9
A	529	ALA	-	expression tag	UNP W8RJF9
A	530	TYR	-	expression tag	UNP W8RJF9
A	531	VAL	-	expression tag	UNP W8RJF9
A	532	ARG	-	expression tag	UNP W8RJF9
A	533	LYS	-	expression tag	UNP W8RJF9
A	534	ASP	-	expression tag	UNP W8RJF9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	535	GLY	-	expression tag	UNP W8RJF9
A	536	GLU	-	expression tag	UNP W8RJF9
A	537	TRP	-	expression tag	UNP W8RJF9
A	538	VAL	-	expression tag	UNP W8RJF9
A	539	LEU	-	expression tag	UNP W8RJF9
A	540	LEU	-	expression tag	UNP W8RJF9
A	541	SER	-	expression tag	UNP W8RJF9
A	542	THR	-	expression tag	UNP W8RJF9
A	543	PHE	-	expression tag	UNP W8RJF9
A	544	LEU	-	expression tag	UNP W8RJF9
A	545	GLY	-	expression tag	UNP W8RJF9
A	546	SER	-	expression tag	UNP W8RJF9
A	547	LEU	-	expression tag	UNP W8RJF9
A	548	GLU	-	expression tag	UNP W8RJF9
A	549	VAL	-	expression tag	UNP W8RJF9
A	550	LEU	-	expression tag	UNP W8RJF9
A	551	PHE	-	expression tag	UNP W8RJF9
A	552	GLN	-	expression tag	UNP W8RJF9
A	553	GLY	-	expression tag	UNP W8RJF9
A	554	PRO	-	expression tag	UNP W8RJF9
A	555	GLY	-	expression tag	UNP W8RJF9
A	556	HIS	-	expression tag	UNP W8RJF9
A	557	HIS	-	expression tag	UNP W8RJF9
A	558	HIS	-	expression tag	UNP W8RJF9
A	559	HIS	-	expression tag	UNP W8RJF9
A	560	HIS	-	expression tag	UNP W8RJF9
A	561	HIS	-	expression tag	UNP W8RJF9
A	562	HIS	-	expression tag	UNP W8RJF9
A	563	HIS	-	expression tag	UNP W8RJF9
A	564	SER	-	expression tag	UNP W8RJF9
A	565	ALA	-	expression tag	UNP W8RJF9
A	566	TRP	-	expression tag	UNP W8RJF9
A	567	SER	-	expression tag	UNP W8RJF9
A	568	HIS	-	expression tag	UNP W8RJF9
A	569	PRO	-	expression tag	UNP W8RJF9
A	570	GLN	-	expression tag	UNP W8RJF9
A	571	PHE	-	expression tag	UNP W8RJF9
A	572	GLU	-	expression tag	UNP W8RJF9
A	573	LYS	-	expression tag	UNP W8RJF9
B	66	GLU	LYS	conflict	UNP W8RJF9
B	67	ILE	ASN	engineered mutation	UNP W8RJF9
B	215	PRO	SER	engineered mutation	UNP W8RJF9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	514	SER	-	expression tag	UNP W8RJF9
B	515	ALA	-	expression tag	UNP W8RJF9
B	516	ILE	-	expression tag	UNP W8RJF9
B	517	GLY	-	expression tag	UNP W8RJF9
B	518	GLY	-	expression tag	UNP W8RJF9
B	519	TYR	-	expression tag	UNP W8RJF9
B	520	ILE	-	expression tag	UNP W8RJF9
B	521	PRO	-	expression tag	UNP W8RJF9
B	522	GLU	-	expression tag	UNP W8RJF9
B	523	ALA	-	expression tag	UNP W8RJF9
B	524	PRO	-	expression tag	UNP W8RJF9
B	525	ARG	-	expression tag	UNP W8RJF9
B	526	ASP	-	expression tag	UNP W8RJF9
B	527	GLY	-	expression tag	UNP W8RJF9
B	528	GLN	-	expression tag	UNP W8RJF9
B	529	ALA	-	expression tag	UNP W8RJF9
B	530	TYR	-	expression tag	UNP W8RJF9
B	531	VAL	-	expression tag	UNP W8RJF9
B	532	ARG	-	expression tag	UNP W8RJF9
B	533	LYS	-	expression tag	UNP W8RJF9
B	534	ASP	-	expression tag	UNP W8RJF9
B	535	GLY	-	expression tag	UNP W8RJF9
B	536	GLU	-	expression tag	UNP W8RJF9
B	537	TRP	-	expression tag	UNP W8RJF9
B	538	VAL	-	expression tag	UNP W8RJF9
B	539	LEU	-	expression tag	UNP W8RJF9
B	540	LEU	-	expression tag	UNP W8RJF9
B	541	SER	-	expression tag	UNP W8RJF9
B	542	THR	-	expression tag	UNP W8RJF9
B	543	PHE	-	expression tag	UNP W8RJF9
B	544	LEU	-	expression tag	UNP W8RJF9
B	545	GLY	-	expression tag	UNP W8RJF9
B	546	SER	-	expression tag	UNP W8RJF9
B	547	LEU	-	expression tag	UNP W8RJF9
B	548	GLU	-	expression tag	UNP W8RJF9
B	549	VAL	-	expression tag	UNP W8RJF9
B	550	LEU	-	expression tag	UNP W8RJF9
B	551	PHE	-	expression tag	UNP W8RJF9
B	552	GLN	-	expression tag	UNP W8RJF9
B	553	GLY	-	expression tag	UNP W8RJF9
B	554	PRO	-	expression tag	UNP W8RJF9
B	555	GLY	-	expression tag	UNP W8RJF9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	556	HIS	-	expression tag	UNP W8RJF9
B	557	HIS	-	expression tag	UNP W8RJF9
B	558	HIS	-	expression tag	UNP W8RJF9
B	559	HIS	-	expression tag	UNP W8RJF9
B	560	HIS	-	expression tag	UNP W8RJF9
B	561	HIS	-	expression tag	UNP W8RJF9
B	562	HIS	-	expression tag	UNP W8RJF9
B	563	HIS	-	expression tag	UNP W8RJF9
B	564	SER	-	expression tag	UNP W8RJF9
B	565	ALA	-	expression tag	UNP W8RJF9
B	566	TRP	-	expression tag	UNP W8RJF9
B	567	SER	-	expression tag	UNP W8RJF9
B	568	HIS	-	expression tag	UNP W8RJF9
B	569	PRO	-	expression tag	UNP W8RJF9
B	570	GLN	-	expression tag	UNP W8RJF9
B	571	PHE	-	expression tag	UNP W8RJF9
B	572	GLU	-	expression tag	UNP W8RJF9
B	573	LYS	-	expression tag	UNP W8RJF9
C	66	GLU	LYS	conflict	UNP W8RJF9
C	67	ILE	ASN	engineered mutation	UNP W8RJF9
C	215	PRO	SER	engineered mutation	UNP W8RJF9
C	514	SER	-	expression tag	UNP W8RJF9
C	515	ALA	-	expression tag	UNP W8RJF9
C	516	ILE	-	expression tag	UNP W8RJF9
C	517	GLY	-	expression tag	UNP W8RJF9
C	518	GLY	-	expression tag	UNP W8RJF9
C	519	TYR	-	expression tag	UNP W8RJF9
C	520	ILE	-	expression tag	UNP W8RJF9
C	521	PRO	-	expression tag	UNP W8RJF9
C	522	GLU	-	expression tag	UNP W8RJF9
C	523	ALA	-	expression tag	UNP W8RJF9
C	524	PRO	-	expression tag	UNP W8RJF9
C	525	ARG	-	expression tag	UNP W8RJF9
C	526	ASP	-	expression tag	UNP W8RJF9
C	527	GLY	-	expression tag	UNP W8RJF9
C	528	GLN	-	expression tag	UNP W8RJF9
C	529	ALA	-	expression tag	UNP W8RJF9
C	530	TYR	-	expression tag	UNP W8RJF9
C	531	VAL	-	expression tag	UNP W8RJF9
C	532	ARG	-	expression tag	UNP W8RJF9
C	533	LYS	-	expression tag	UNP W8RJF9
C	534	ASP	-	expression tag	UNP W8RJF9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	535	GLY	-	expression tag	UNP W8RJF9
C	536	GLU	-	expression tag	UNP W8RJF9
C	537	TRP	-	expression tag	UNP W8RJF9
C	538	VAL	-	expression tag	UNP W8RJF9
C	539	LEU	-	expression tag	UNP W8RJF9
C	540	LEU	-	expression tag	UNP W8RJF9
C	541	SER	-	expression tag	UNP W8RJF9
C	542	THR	-	expression tag	UNP W8RJF9
C	543	PHE	-	expression tag	UNP W8RJF9
C	544	LEU	-	expression tag	UNP W8RJF9
C	545	GLY	-	expression tag	UNP W8RJF9
C	546	SER	-	expression tag	UNP W8RJF9
C	547	LEU	-	expression tag	UNP W8RJF9
C	548	GLU	-	expression tag	UNP W8RJF9
C	549	VAL	-	expression tag	UNP W8RJF9
C	550	LEU	-	expression tag	UNP W8RJF9
C	551	PHE	-	expression tag	UNP W8RJF9
C	552	GLN	-	expression tag	UNP W8RJF9
C	553	GLY	-	expression tag	UNP W8RJF9
C	554	PRO	-	expression tag	UNP W8RJF9
C	555	GLY	-	expression tag	UNP W8RJF9
C	556	HIS	-	expression tag	UNP W8RJF9
C	557	HIS	-	expression tag	UNP W8RJF9
C	558	HIS	-	expression tag	UNP W8RJF9
C	559	HIS	-	expression tag	UNP W8RJF9
C	560	HIS	-	expression tag	UNP W8RJF9
C	561	HIS	-	expression tag	UNP W8RJF9
C	562	HIS	-	expression tag	UNP W8RJF9
C	563	HIS	-	expression tag	UNP W8RJF9
C	564	SER	-	expression tag	UNP W8RJF9
C	565	ALA	-	expression tag	UNP W8RJF9
C	566	TRP	-	expression tag	UNP W8RJF9
C	567	SER	-	expression tag	UNP W8RJF9
C	568	HIS	-	expression tag	UNP W8RJF9
C	569	PRO	-	expression tag	UNP W8RJF9
C	570	GLN	-	expression tag	UNP W8RJF9
C	571	PHE	-	expression tag	UNP W8RJF9
C	572	GLU	-	expression tag	UNP W8RJF9
C	573	LYS	-	expression tag	UNP W8RJF9

- Molecule 2 is a protein called Heavy chain of human antibody Fab ADI-14442.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	111	Total	C	N	O	S	0	0
			848	536	142	165	5		
2	I	111	Total	C	N	O	S	0	0
			848	536	142	165	5		
2	J	111	Total	C	N	O	S	0	0
			848	536	142	165	5		

- Molecule 3 is a protein called Light chain of human antibody Fab ADI-14442.

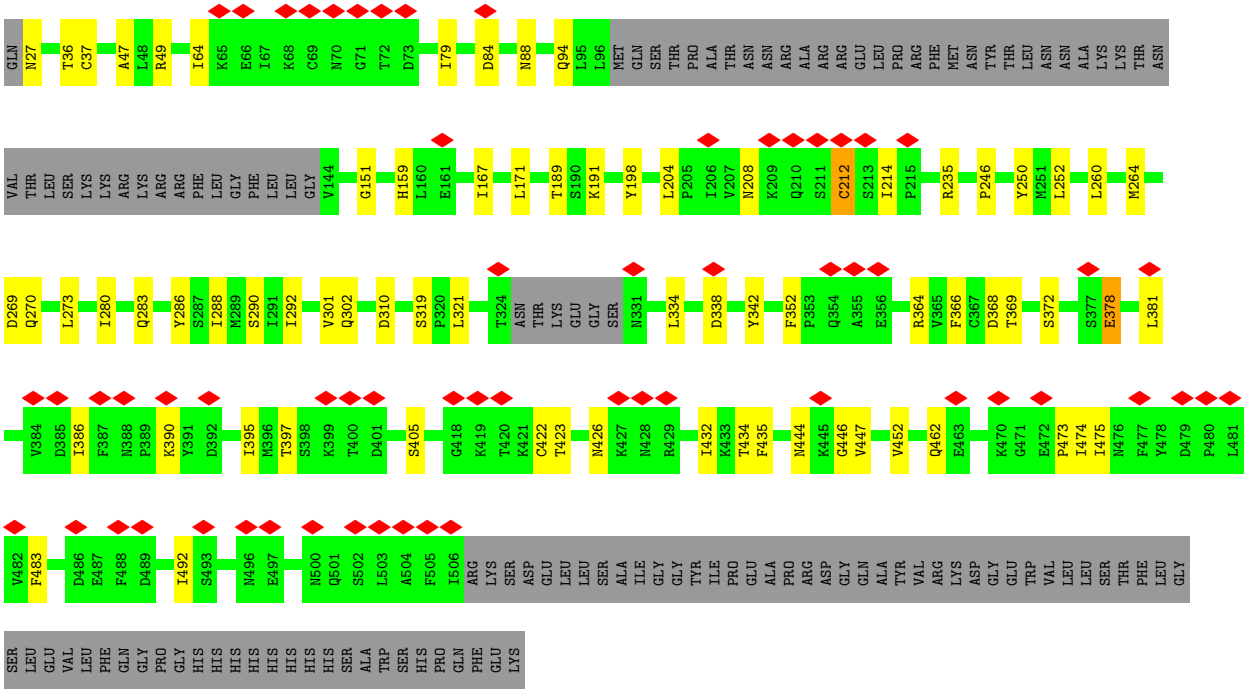
Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	111	Total	C	N	O	S	0	0
			858	536	153	165	4		
3	M	111	Total	C	N	O	S	0	0
			858	536	153	165	4		
3	N	111	Total	C	N	O	S	0	0
			858	536	153	165	4		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

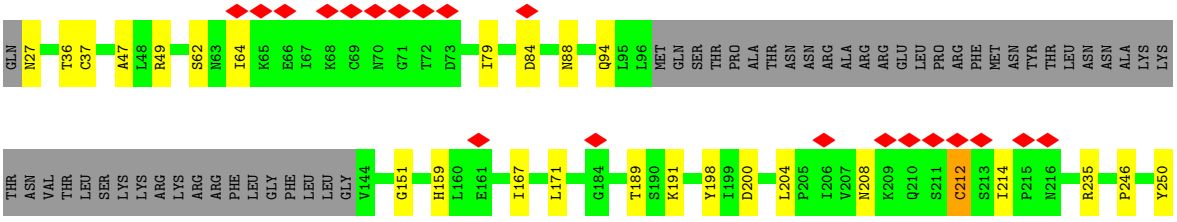
• Molecule 1: Fusion glycoprotein F0

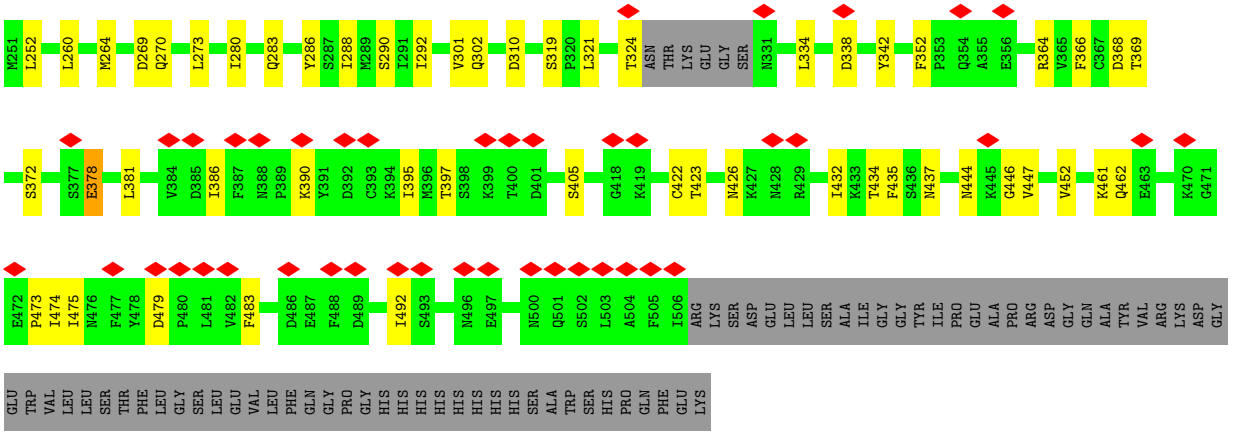
Chain A:



• Molecule 1: Fusion glycoprotein F0

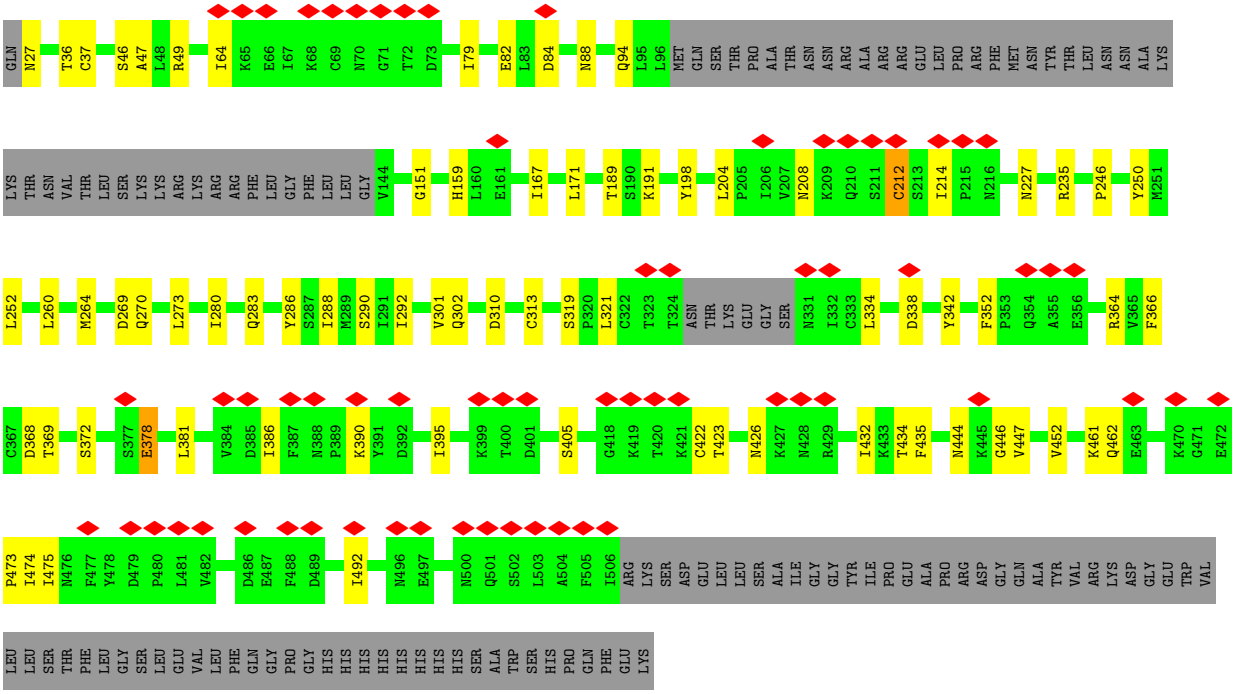
Chain B:





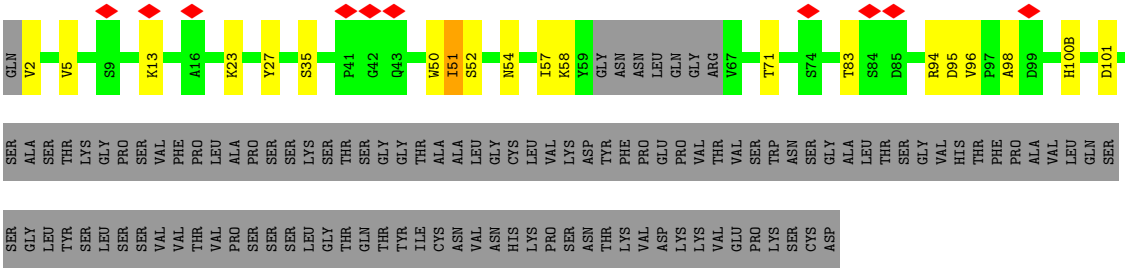
• Molecule 1: Fusion glycoprotein F0

Chain C:



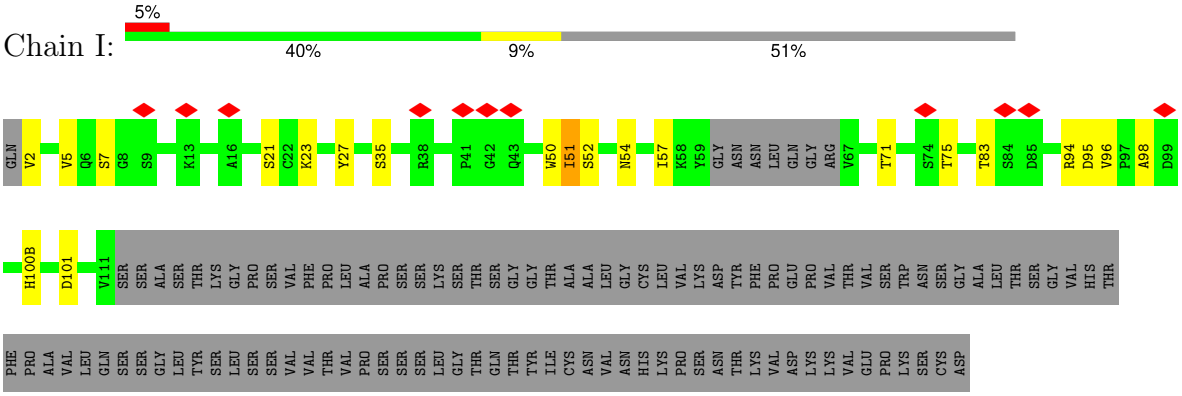
• Molecule 2: Heavy chain of human antibody Fab ADI-14442

Chain H:



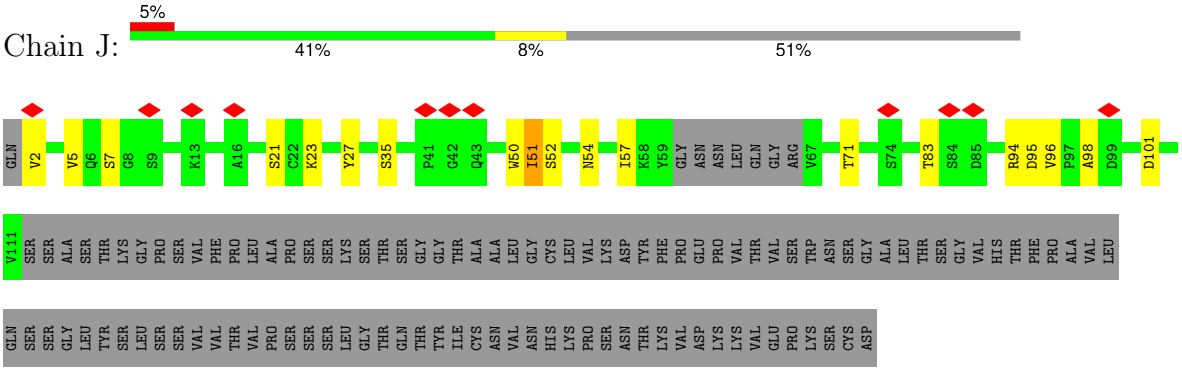
• Molecule 2: Heavy chain of human antibody Fab ADI-14442

Chain I:



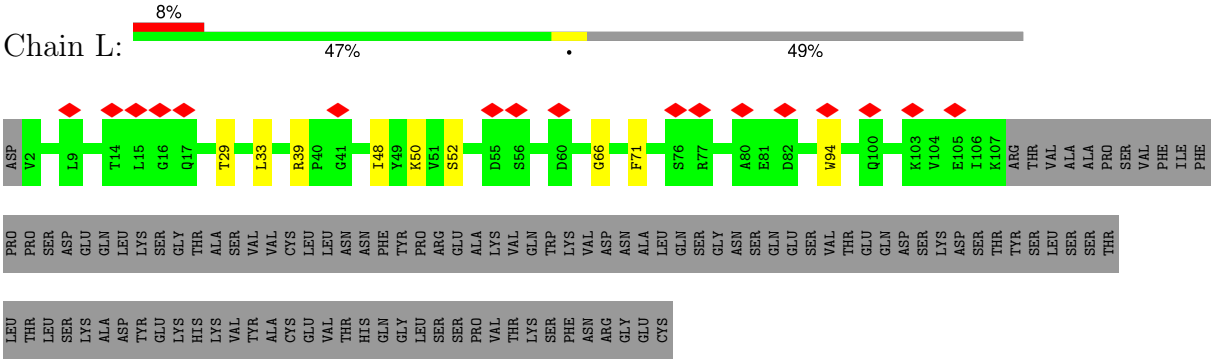
• Molecule 2: Heavy chain of human antibody Fab ADI-14442

Chain J:



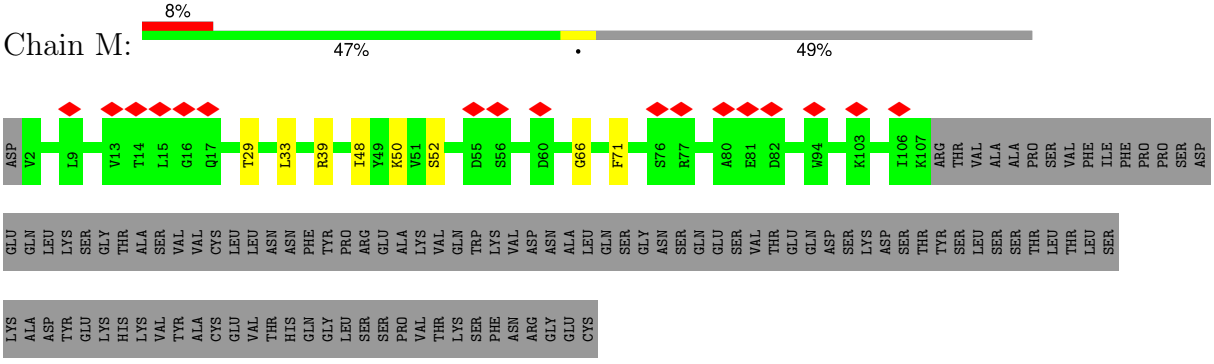
• Molecule 3: Light chain of human antibody Fab ADI-14442

Chain L:



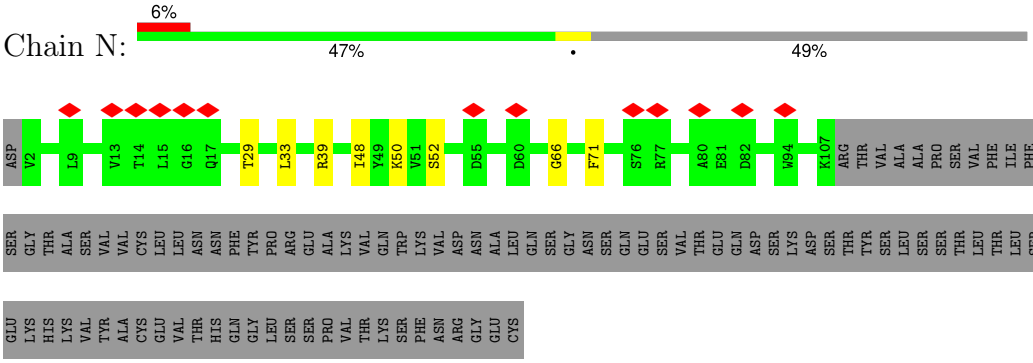
• Molecule 3: Light chain of human antibody Fab ADI-14442

Chain M:



• Molecule 3: Light chain of human antibody Fab ADI-14442

Chain N:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	371323	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	48	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.242	Depositor
Minimum map value	-0.169	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	322.5, 322.5, 322.5	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.075, 1.075, 1.075	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.26	0/3347	0.42	0/4540
1	B	0.26	0/3347	0.42	0/4540
1	C	0.26	0/3347	0.42	0/4540
2	H	0.28	0/867	0.43	0/1180
2	I	0.27	0/867	0.43	0/1180
2	J	0.27	0/867	0.43	0/1180
3	L	0.26	0/878	0.43	0/1191
3	M	0.26	0/878	0.43	0/1191
3	N	0.26	0/878	0.43	0/1191
All	All	0.26	0/15276	0.42	0/20733

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3300	0	3340	40	0
1	B	3300	0	3340	44	0
1	C	3300	0	3340	42	0
2	H	848	0	814	12	0
2	I	848	0	814	12	0
2	J	848	0	814	11	0
3	L	858	0	840	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	M	858	0	840	4	0
3	N	858	0	840	4	0
All	All	15018	0	14982	167	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (167) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:84:ASP:O	1:B:88:ASN:ND2	2.29	0.65
1:C:84:ASP:O	1:C:88:ASN:ND2	2.29	0.63
2:H:94:ARG:NH2	2:H:101:ASP:OD2	2.31	0.62
2:I:94:ARG:NH2	2:I:101:ASP:OD2	2.30	0.62
1:A:198:TYR:HB2	3:L:29:THR:HG21	1.81	0.62
2:J:94:ARG:NH2	2:J:101:ASP:OD2	2.31	0.61
2:J:7:SER:HG	2:J:21:SER:HG	1.46	0.60
1:A:84:ASP:O	1:A:88:ASN:ND2	2.29	0.60
1:C:198:TYR:HB2	3:N:29:THR:HG21	1.85	0.58
2:I:96:VAL:HG22	2:I:98:ALA:H	1.70	0.57
2:H:96:VAL:HG22	2:H:98:ALA:H	1.70	0.57
1:B:334:LEU:HB2	1:B:475:ILE:HD13	1.87	0.56
2:J:96:VAL:HG22	2:J:98:ALA:H	1.70	0.56
1:C:334:LEU:HB2	1:C:475:ILE:HD13	1.87	0.56
1:C:310:ASP:OD1	1:C:364:ARG:NH1	2.34	0.56
1:A:334:LEU:HB2	1:A:475:ILE:HD13	1.87	0.56
1:B:426:ASN:ND2	1:B:446:GLY:O	2.25	0.55
1:C:444:ASN:ND2	1:C:462:GLN:O	2.40	0.55
2:H:101:ASP:N	2:H:101:ASP:OD1	2.40	0.55
1:A:49:ARG:O	1:A:369:THR:OG1	2.20	0.55
1:B:321:LEU:HD11	1:B:473:PRO:HB3	1.89	0.55
1:B:198:TYR:HB2	3:M:29:THR:HG21	1.88	0.55
1:C:321:LEU:HD11	1:C:473:PRO:HB3	1.89	0.55
1:B:444:ASN:ND2	1:B:462:GLN:O	2.40	0.54
1:A:321:LEU:HD11	1:A:473:PRO:HB3	1.89	0.54
1:A:426:ASN:ND2	1:A:446:GLY:O	2.25	0.54
1:A:444:ASN:ND2	1:A:462:GLN:O	2.40	0.54
2:I:35:SER:OG	2:I:95:ASP:OD2	2.24	0.54
1:B:352:PHE:CE2	1:B:372:SER:HB2	2.43	0.54
2:I:7:SER:OG	2:I:21:SER:OG	2.21	0.54
1:C:352:PHE:CE2	1:C:372:SER:HB2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:310:ASP:OD1	1:B:364:ARG:NH1	2.34	0.53
1:A:405:SER:HB3	1:A:452:VAL:HG21	1.90	0.53
3:M:66:GLY:HA3	3:M:71:PHE:HA	1.91	0.53
1:A:235:ARG:NH1	1:B:250:TYR:OH	2.42	0.53
1:A:352:PHE:CE2	1:A:372:SER:HB2	2.43	0.53
3:N:66:GLY:HA3	3:N:71:PHE:HA	1.91	0.53
3:L:50:LYS:O	3:L:52:SER:N	2.42	0.52
1:B:151:GLY:HA3	1:B:288:ILE:HD13	1.91	0.52
1:A:151:GLY:HA3	1:A:288:ILE:HD13	1.91	0.52
1:B:405:SER:HB3	1:B:452:VAL:HG21	1.90	0.52
3:M:50:LYS:O	3:M:52:SER:N	2.42	0.52
1:C:151:GLY:HA3	1:C:288:ILE:HD13	1.92	0.52
1:C:405:SER:HB3	1:C:452:VAL:HG21	1.90	0.52
2:J:35:SER:OG	2:J:95:ASP:OD2	2.24	0.52
3:N:50:LYS:O	3:N:52:SER:N	2.42	0.52
1:A:250:TYR:OH	1:C:235:ARG:NH1	2.43	0.52
3:L:66:GLY:HA3	3:L:71:PHE:HA	1.91	0.52
1:A:280:ILE:HG21	1:A:366:PHE:CG	2.45	0.52
2:H:51:ILE:HD12	2:H:57:ILE:HG12	1.92	0.52
2:I:51:ILE:HD12	2:I:57:ILE:HG12	1.92	0.52
1:B:280:ILE:HG21	1:B:366:PHE:CG	2.45	0.51
2:I:101:ASP:N	2:I:101:ASP:OD1	2.40	0.51
1:B:235:ARG:NH1	1:C:250:TYR:OH	2.43	0.51
1:C:280:ILE:HG21	1:C:366:PHE:CG	2.45	0.51
1:C:171:LEU:HD13	1:C:191:LYS:HB2	1.93	0.51
1:A:171:LEU:HD13	1:A:191:LYS:HB2	1.93	0.50
2:J:51:ILE:HD12	2:J:57:ILE:HG12	1.92	0.50
1:A:422:CYS:HB2	1:A:435:PHE:HB2	1.93	0.50
2:J:101:ASP:OD1	2:J:101:ASP:N	2.40	0.50
1:B:171:LEU:HD13	1:B:191:LYS:HB2	1.93	0.50
2:H:35:SER:OG	2:H:95:ASP:OD2	2.24	0.50
1:B:422:CYS:HB2	1:B:435:PHE:HB2	1.93	0.50
1:C:422:CYS:HB2	1:C:435:PHE:HB2	1.93	0.49
1:C:426:ASN:ND2	1:C:446:GLY:O	2.25	0.49
2:H:5:VAL:HG23	2:H:23:LYS:HB3	1.95	0.48
1:C:159:HIS:NE2	1:C:290:SER:O	2.47	0.48
1:A:432:ILE:HD11	1:A:447:VAL:HG22	1.95	0.48
1:A:159:HIS:NE2	1:A:290:SER:O	2.47	0.48
1:B:159:HIS:NE2	1:B:290:SER:O	2.47	0.48
2:J:5:VAL:HG23	2:J:23:LYS:HB3	1.95	0.48
1:A:310:ASP:OD1	1:A:364:ARG:NH1	2.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:ASP:OD1	1:A:270:GLN:N	2.47	0.47
2:I:5:VAL:HG23	2:I:23:LYS:HB3	1.95	0.47
1:B:269:ASP:OD1	1:B:270:GLN:N	2.47	0.47
1:B:432:ILE:HD11	1:B:447:VAL:HG22	1.95	0.47
1:C:94:GLN:HA	1:C:292:ILE:HG21	1.97	0.47
1:C:82:GLU:OE2	1:C:227:ASN:ND2	2.42	0.47
1:C:386:ILE:HG21	1:C:474:ILE:HG21	1.96	0.47
1:C:423:THR:HG22	1:C:434:THR:HG22	1.97	0.47
1:C:432:ILE:HD11	1:C:447:VAL:HG22	1.95	0.47
1:C:269:ASP:OD1	1:C:270:GLN:N	2.47	0.47
1:A:423:THR:HG22	1:A:434:THR:HG22	1.97	0.47
1:C:49:ARG:O	1:C:369:THR:OG1	2.20	0.47
1:B:386:ILE:HG21	1:B:474:ILE:HG21	1.96	0.47
1:B:395:ILE:HD13	1:B:492:ILE:HD13	1.97	0.47
1:A:386:ILE:HG21	1:A:474:ILE:HG21	1.96	0.46
1:C:171:LEU:HD11	1:C:189:THR:HG22	1.98	0.46
1:B:94:GLN:HA	1:B:292:ILE:HG21	1.97	0.46
1:B:423:THR:HG22	1:B:434:THR:HG22	1.97	0.46
1:A:94:GLN:HA	1:A:292:ILE:HG21	1.97	0.46
1:B:49:ARG:O	1:B:369:THR:OG1	2.20	0.46
1:A:171:LEU:HD11	1:A:189:THR:HG22	1.98	0.45
2:I:50:TRP:CZ2	2:I:52:SER:HB2	2.51	0.45
1:B:171:LEU:HD11	1:B:189:THR:HG22	1.98	0.45
1:B:167:ILE:HG23	1:B:189:THR:HG21	1.99	0.45
2:J:50:TRP:CZ2	2:J:52:SER:HB2	2.51	0.45
3:L:48:ILE:HG22	3:L:50:LYS:O	2.17	0.45
1:A:395:ILE:HD13	1:A:492:ILE:HD13	1.97	0.45
1:C:167:ILE:HG23	1:C:189:THR:HG21	1.99	0.45
1:C:378:GLU:HG2	1:C:390:LYS:HB3	1.99	0.45
3:M:48:ILE:HG22	3:M:50:LYS:O	2.17	0.45
1:A:378:GLU:HG2	1:A:390:LYS:HB3	1.99	0.45
1:B:49:ARG:HE	1:B:368:ASP:CG	2.21	0.45
1:C:49:ARG:HE	1:C:368:ASP:CG	2.21	0.44
1:C:395:ILE:HD13	1:C:492:ILE:HD13	1.97	0.44
2:I:51:ILE:HG12	2:I:71:THR:HG23	1.99	0.44
1:A:167:ILE:HG23	1:A:189:THR:HG21	1.99	0.44
2:J:51:ILE:HG12	2:J:71:THR:HG23	1.99	0.44
1:B:378:GLU:HG2	1:B:390:LYS:HB3	1.99	0.44
2:H:50:TRP:CZ2	2:H:52:SER:HB2	2.52	0.44
1:B:444:ASN:O	1:B:461:LYS:NZ	2.46	0.44
2:H:51:ILE:HG12	2:H:71:THR:HG23	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:ARG:HE	1:A:368:ASP:CG	2.21	0.44
1:B:62:SER:OG	1:B:200:ASP:OD1	2.30	0.44
1:B:260:LEU:O	1:B:264:MET:HG3	2.18	0.44
1:B:47:ALA:HB1	1:B:273:LEU:HD21	2.00	0.44
1:C:260:LEU:O	1:C:264:MET:HG3	2.18	0.44
3:N:48:ILE:HG22	3:N:50:LYS:O	2.17	0.43
1:A:260:LEU:O	1:A:264:MET:HG3	2.18	0.43
1:A:208:ASN:O	1:A:212:CYS:N	2.52	0.43
1:B:79:ILE:HG13	1:B:214:ILE:HD12	2.01	0.43
1:C:378:GLU:HA	1:C:381:LEU:HD23	2.01	0.43
1:A:47:ALA:HB1	1:A:273:LEU:HD21	2.00	0.43
1:A:338:ASP:HB2	1:A:342:TYR:OH	2.19	0.43
1:B:64:ILE:HD12	1:B:204:LEU:HD11	2.01	0.43
1:C:338:ASP:HB2	1:C:342:TYR:OH	2.19	0.43
1:A:79:ILE:HG13	1:A:214:ILE:HD12	2.01	0.43
2:I:95:ASP:OD2	2:I:100(B):HIS:ND1	2.42	0.42
1:C:208:ASN:O	1:C:212:CYS:N	2.52	0.42
1:A:36:THR:HG22	1:A:474:ILE:HD13	2.01	0.42
1:C:36:THR:HG22	1:C:474:ILE:HD13	2.00	0.42
1:A:246:PRO:HB3	1:A:283:GLN:HA	2.02	0.42
1:B:338:ASP:HB2	1:B:342:TYR:OH	2.19	0.42
1:B:378:GLU:HA	1:B:381:LEU:HD23	2.01	0.42
1:C:47:ALA:HB1	1:C:273:LEU:HD21	2.00	0.42
2:H:2:VAL:HG13	2:H:27:TYR:CD2	2.55	0.42
1:A:64:ILE:HD12	1:A:204:LEU:HD11	2.01	0.42
1:B:36:THR:HG22	1:B:474:ILE:HD13	2.01	0.42
2:J:2:VAL:HG13	2:J:27:TYR:CD2	2.55	0.42
1:C:246:PRO:HB3	1:C:283:GLN:HA	2.02	0.42
1:C:444:ASN:O	1:C:461:LYS:NZ	2.46	0.42
1:A:37:CYS:SG	1:A:319:SER:HB3	2.60	0.42
1:A:378:GLU:HA	1:A:381:LEU:HD23	2.01	0.41
1:B:37:CYS:SG	1:B:319:SER:HB3	2.60	0.41
1:C:79:ILE:HG13	1:C:214:ILE:HD12	2.01	0.41
2:H:58:LYS:HE3	3:L:94:TRP:CE2	2.55	0.41
2:H:95:ASP:OD2	2:H:100(B):HIS:ND1	2.42	0.41
2:I:2:VAL:HG13	2:I:27:TYR:CD2	2.55	0.41
1:B:246:PRO:HB3	1:B:283:GLN:HA	2.02	0.41
1:C:37:CYS:SG	1:C:319:SER:HB3	2.60	0.41
1:A:286:TYR:HB2	1:A:302:GLN:HE21	1.85	0.41
2:J:7:SER:OG	2:J:21:SER:OG	2.21	0.41
1:C:64:ILE:HD12	1:C:204:LEU:HD11	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:208:ASN:O	1:B:212:CYS:N	2.52	0.41
1:C:286:TYR:HB2	1:C:302:GLN:HE21	1.85	0.41
1:C:252:LEU:HD22	1:C:301:VAL:HG11	2.03	0.41
1:C:46:SER:HB3	1:C:313:CYS:SG	2.62	0.41
1:A:397:THR:HB	1:A:483:PHE:CE2	2.57	0.40
1:B:252:LEU:HD22	1:B:301:VAL:HG11	2.03	0.40
1:B:324:THR:HG21	1:B:437:ASN:HB3	2.03	0.40
1:B:397:THR:HB	1:B:483:PHE:CE2	2.56	0.40
1:B:479:ASP:OD1	1:B:479:ASP:N	2.55	0.40
1:A:252:LEU:HD22	1:A:301:VAL:HG11	2.03	0.40
1:B:286:TYR:HB2	1:B:302:GLN:HE21	1.85	0.40
2:I:23:LYS:NZ	2:I:75:THR:O	2.37	0.40
2:H:13:LYS:HD3	2:H:13:LYS:HA	1.97	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	421/548 (77%)	412 (98%)	9 (2%)	0	100	100
1	B	421/548 (77%)	412 (98%)	9 (2%)	0	100	100
1	C	421/548 (77%)	412 (98%)	9 (2%)	0	100	100
2	H	107/225 (48%)	107 (100%)	0	0	100	100
2	I	107/225 (48%)	107 (100%)	0	0	100	100
2	J	107/225 (48%)	107 (100%)	0	0	100	100
3	L	109/219 (50%)	107 (98%)	2 (2%)	0	100	100
3	M	109/219 (50%)	107 (98%)	2 (2%)	0	100	100
3	N	109/219 (50%)	107 (98%)	2 (2%)	0	100	100
All	All	1911/2976 (64%)	1878 (98%)	33 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	390/495 (79%)	387 (99%)	3 (1%)	79	93
1	B	390/495 (79%)	387 (99%)	3 (1%)	79	93
1	C	390/495 (79%)	387 (99%)	3 (1%)	79	93
2	H	91/189 (48%)	88 (97%)	3 (3%)	33	68
2	I	91/189 (48%)	88 (97%)	3 (3%)	33	68
2	J	91/189 (48%)	88 (97%)	3 (3%)	33	68
3	L	98/195 (50%)	96 (98%)	2 (2%)	50	79
3	M	98/195 (50%)	96 (98%)	2 (2%)	50	79
3	N	98/195 (50%)	96 (98%)	2 (2%)	50	79
All	All	1737/2637 (66%)	1713 (99%)	24 (1%)	62	86

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	ASN
1	A	212	CYS
1	A	378	GLU
1	B	27	ASN
1	B	212	CYS
1	B	378	GLU
1	C	27	ASN
1	C	212	CYS
1	C	378	GLU
2	H	51	ILE
2	H	54	ASN
2	H	83	THR
2	I	51	ILE
2	I	54	ASN
2	I	83	THR

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Mol	Chain	Res	Type
2	J	51	ILE
2	J	54	ASN
2	J	83	THR
3	L	33	LEU
3	L	39	ARG
3	M	33	LEU
3	M	39	ARG
3	N	33	LEU
3	N	39	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

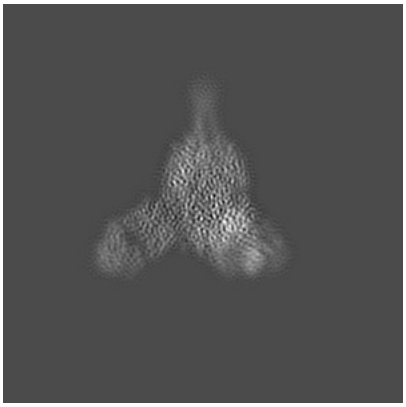
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-23521. These allow visual inspection of the internal detail of the map and identification of artifacts.

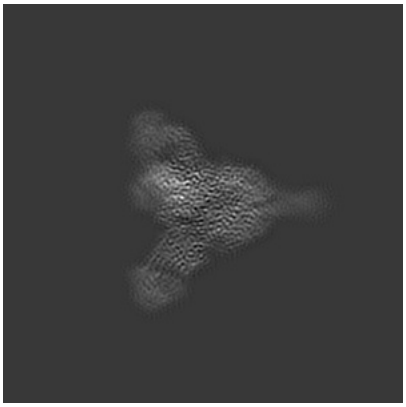
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

6.1.1 Primary map



X



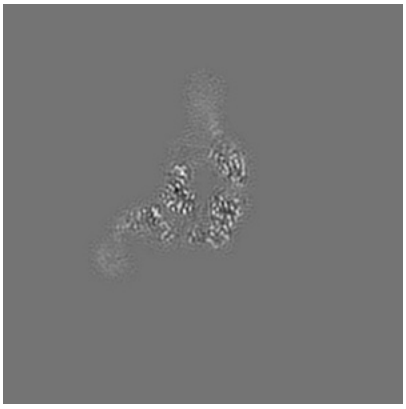
Y

Z

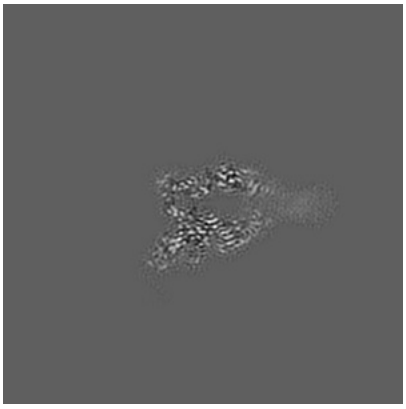
The images above show the map projected in three orthogonal directions.

6.2 Central slices

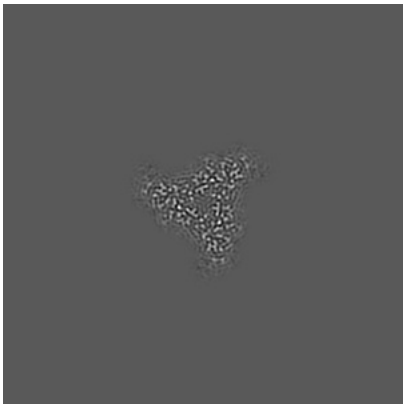
6.2.1 Primary map



X Index: 150



Y Index: 150



Z Index: 150

The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 162

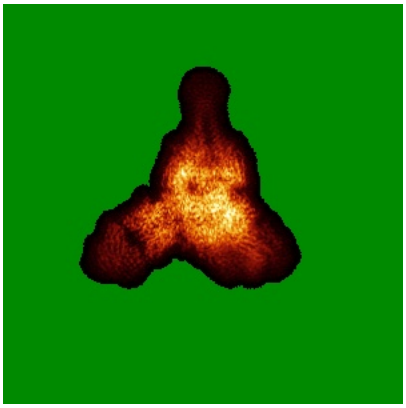
Y Index: 167

Z Index: 145

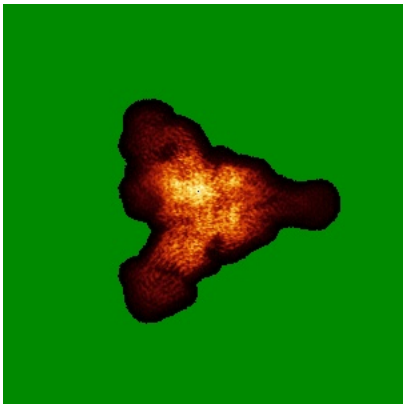
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

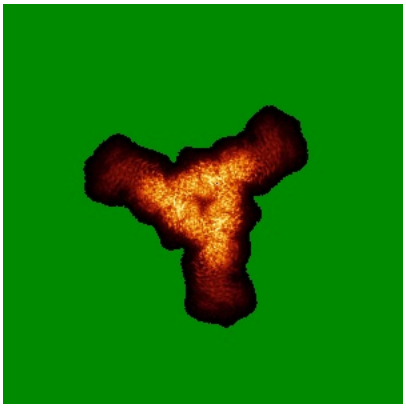
6.4.1 Primary map



X



Y

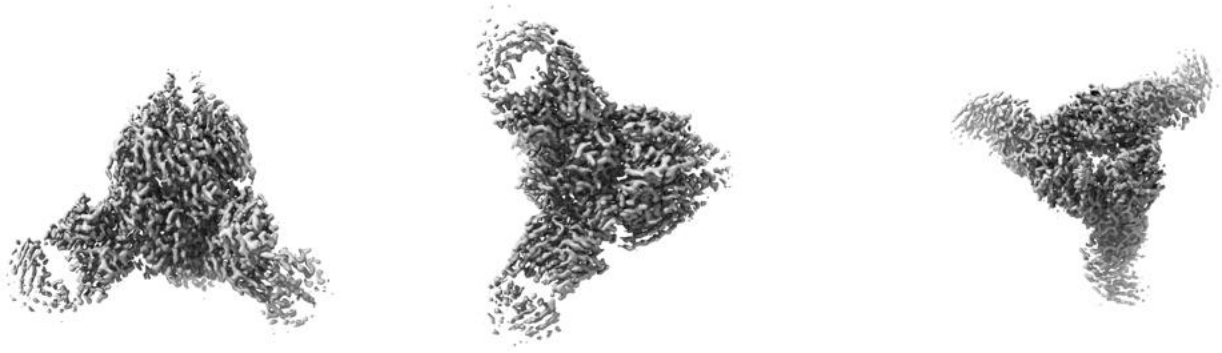


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

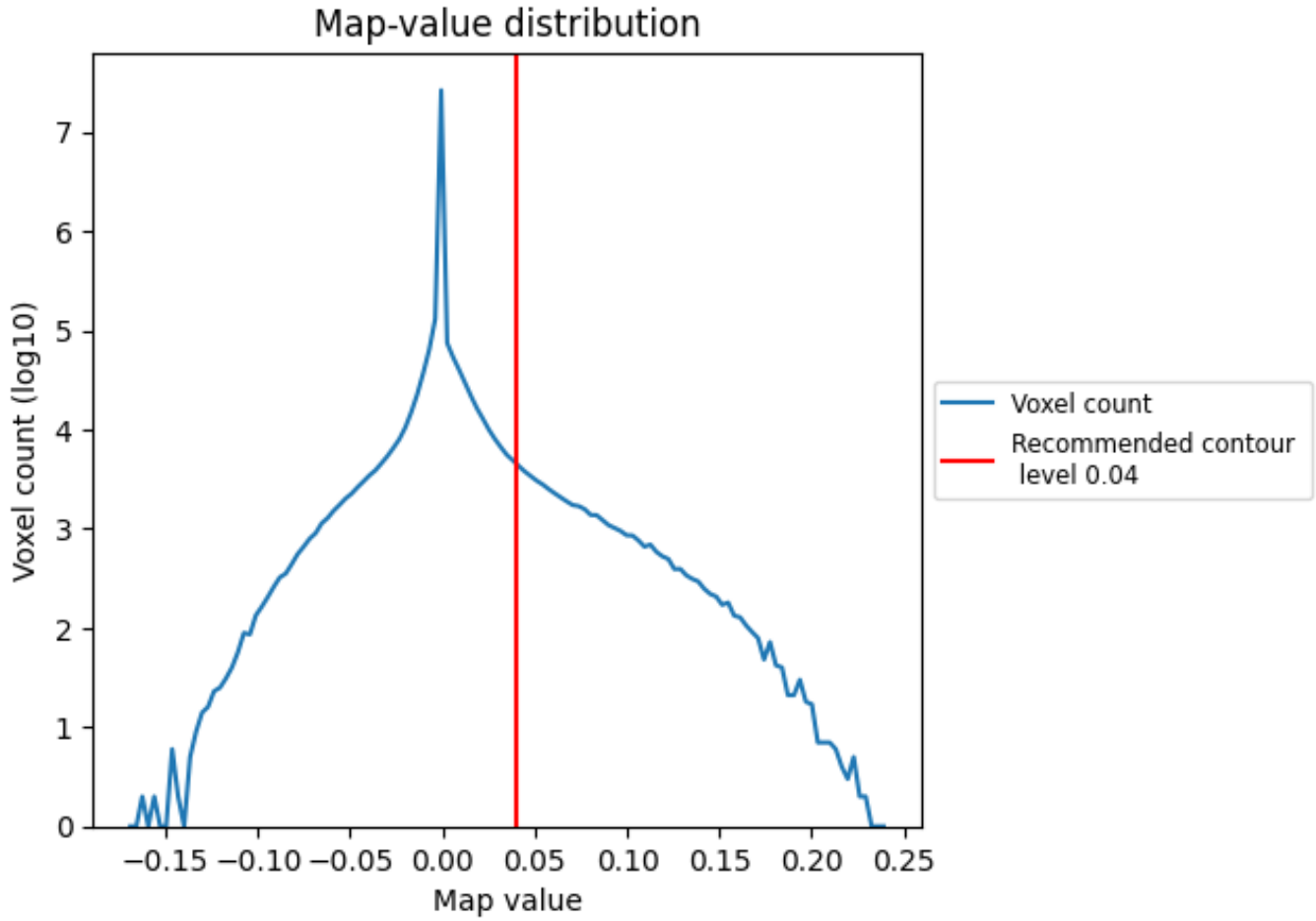
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

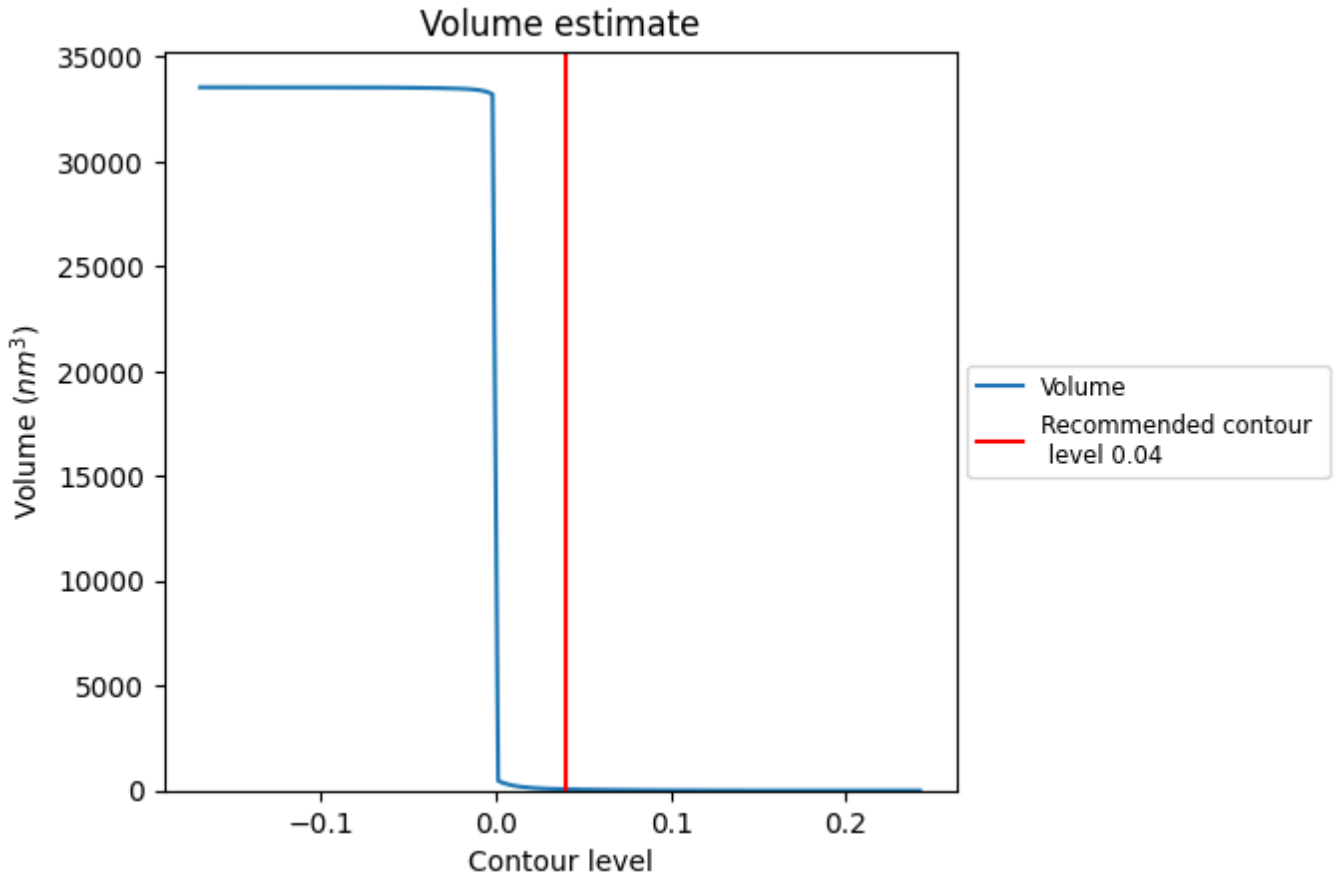
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

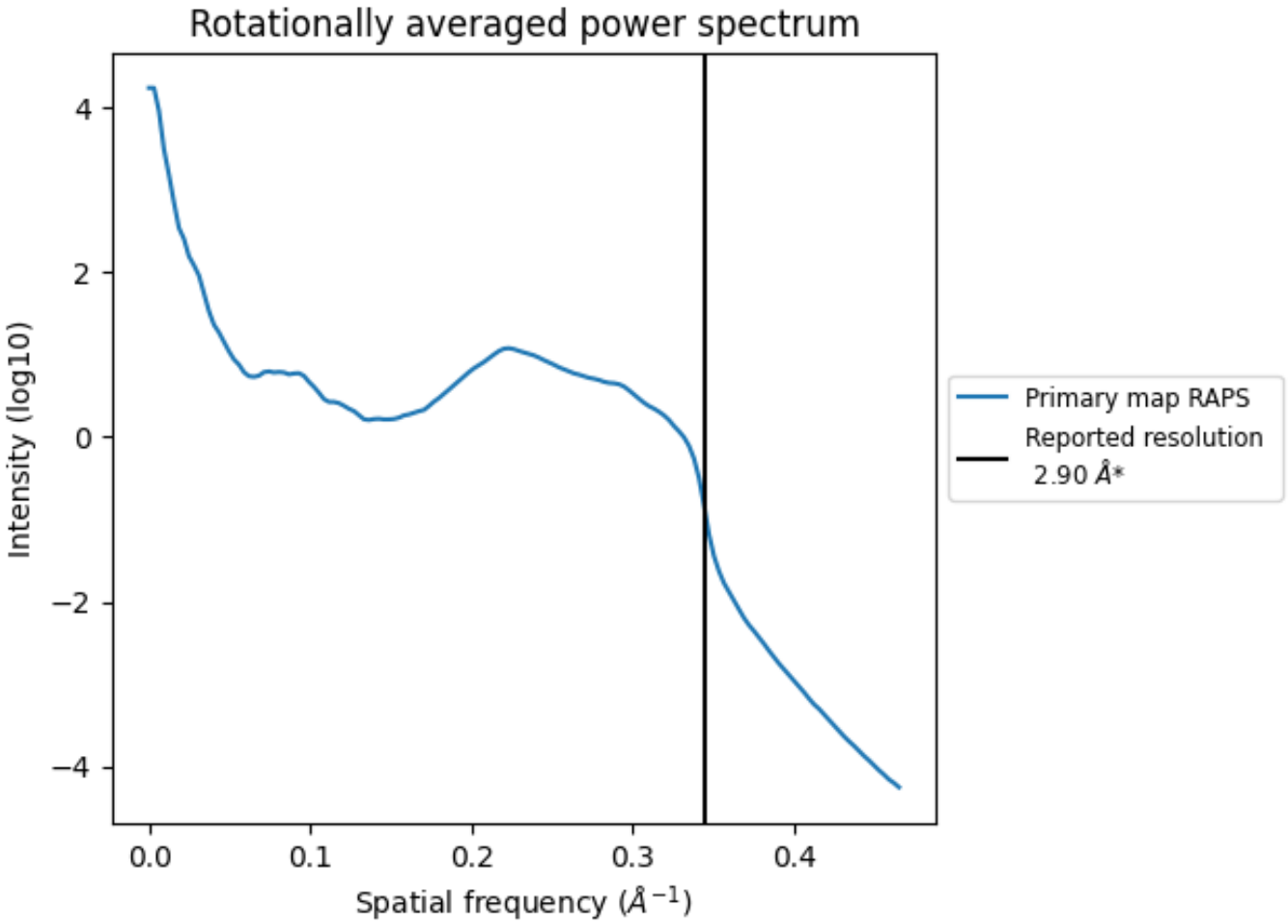
7.2 Volume estimate



The volume at the recommended contour level is 61 nm^3; this corresponds to an approximate mass of 55 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

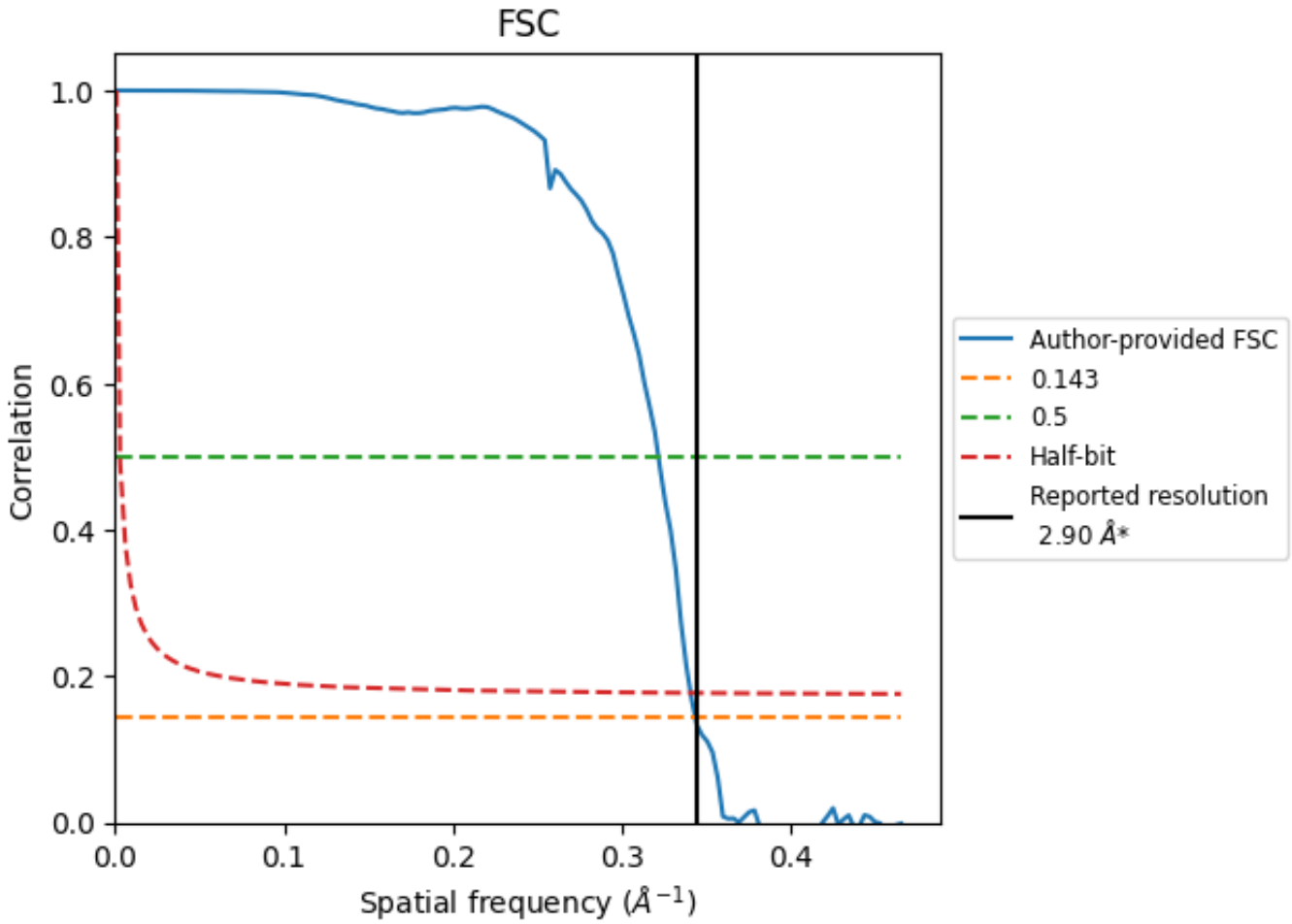


*Reported resolution corresponds to spatial frequency of 0.345 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.345 Å^{-1}

8.2 Resolution estimates (i)

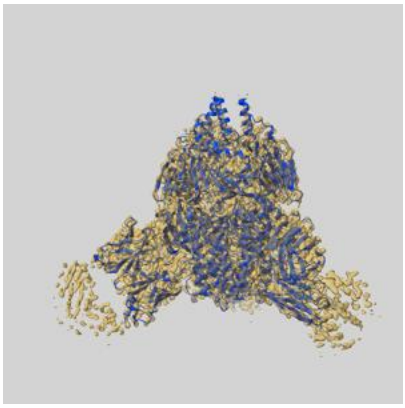
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.91	3.11	2.94
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

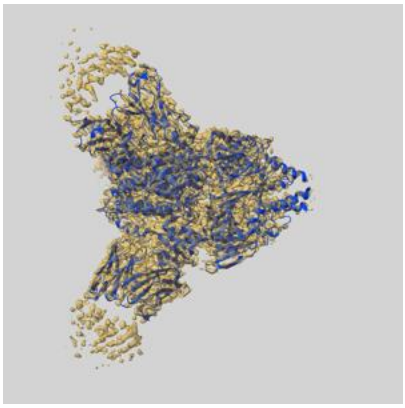
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-23521 and PDB model 7LUE. Per-residue inclusion information can be found in section 3 on page 10.

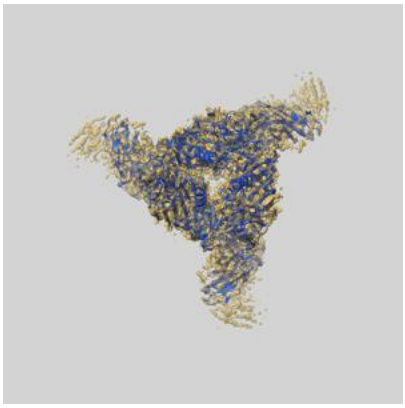
9.1 Map-model overlay



X



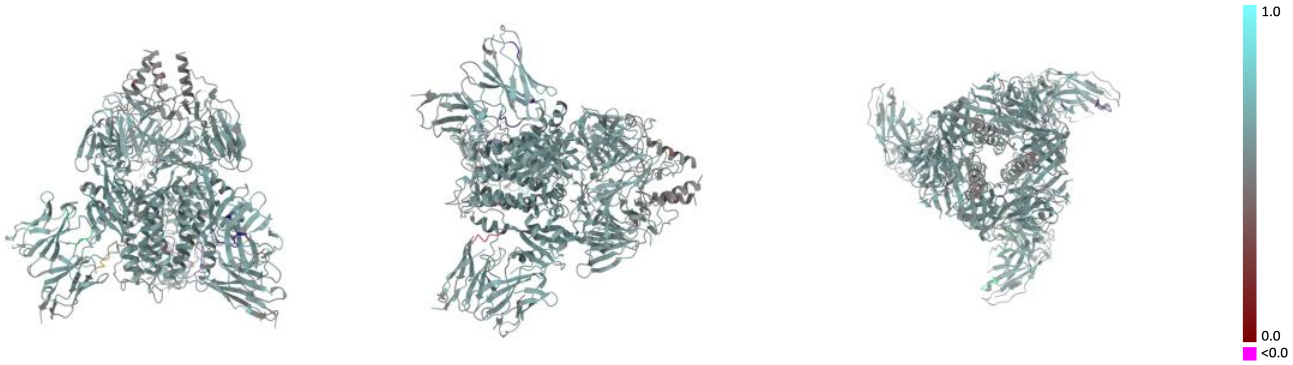
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

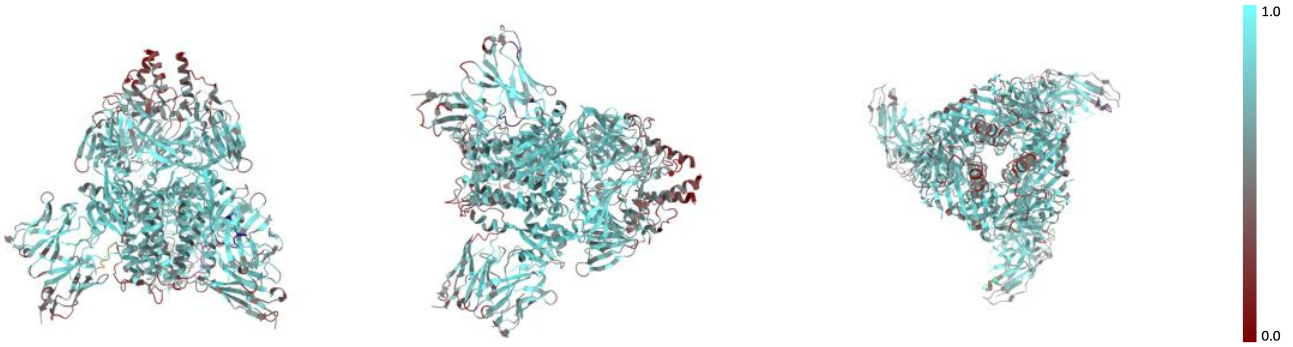
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

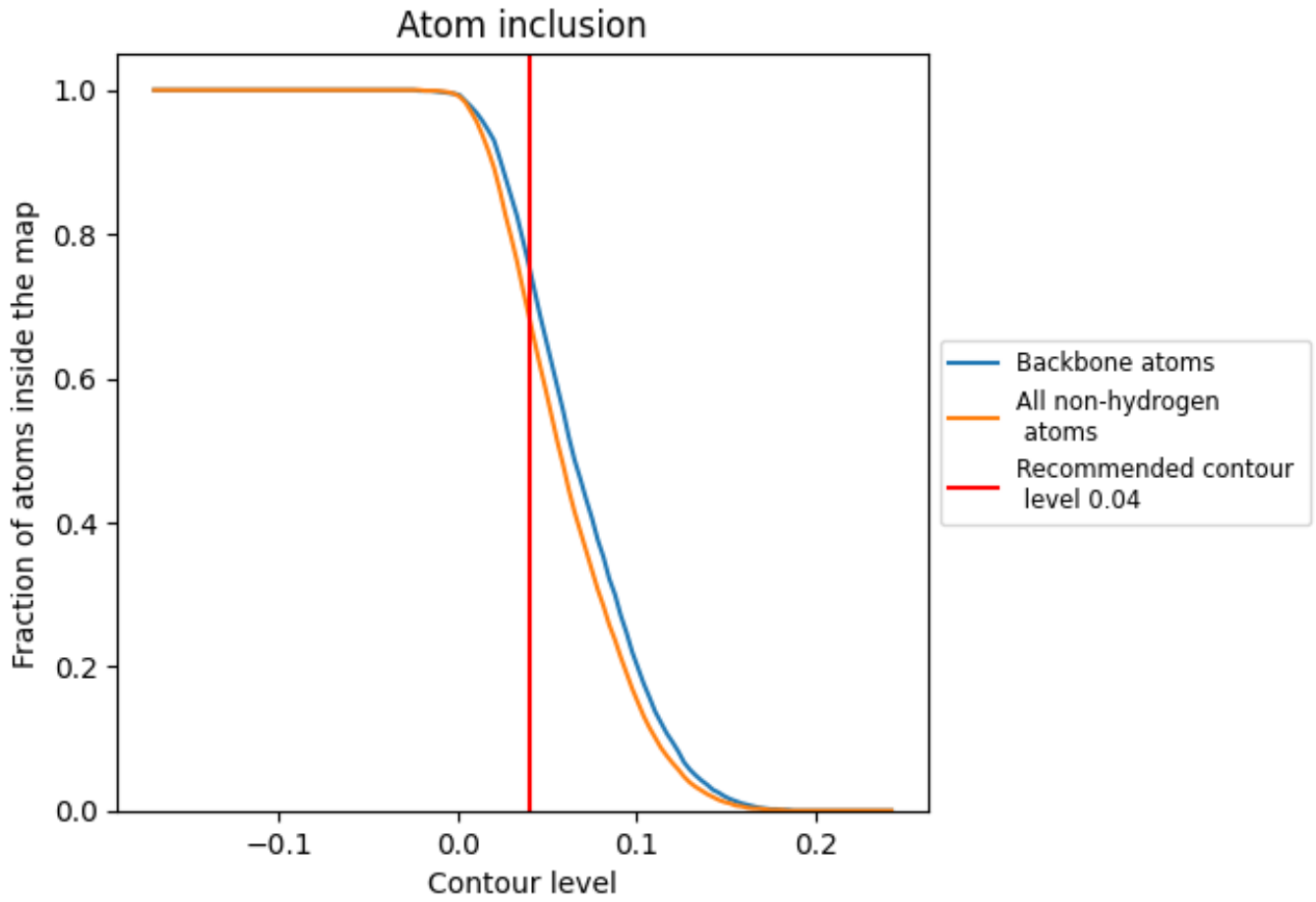
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).

9.4 Atom inclusion (i)



At the recommended contour level, 76% of all backbone atoms, 69% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6860	0.5720
A	0.6800	0.5720
B	0.6790	0.5720
C	0.6780	0.5700
H	0.7260	0.5850
I	0.7200	0.5840
J	0.7270	0.5820
L	0.6740	0.5660
M	0.6710	0.5650
N	0.6740	0.5630